

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Su, Michael Shin-San
Fox, Ted
Wilson, Keith Phillip
Germann, Ursula A.
- (ii) TITLE OF INVENTION: Methods For Designing Inhibitors of
Serine/Thereonine Kinases and Tyrosine Kinase
- 10 (iii) NUMBER OF SEQUENCES: 37
- (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Fish & Neave
(B) STREET: 1251 Avenue of the Americas
(C) CITY: New York
(D) STATE: NY
(E) COUNTRY: US
(F) ZIP: 10020
- 20 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 25 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- 30 (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Haley, James F.
(B) REGISTRATION NUMBER: 27,794
(C) REFERENCE/DOCKET NUMBER: VPI 97-104
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 596-9000
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35 (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 360 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr
1 5 10 15

	Ile	Trp	Glu	Val	Pro	Glu	Arg	Tyr	Gln	Asn	Leu	Ser	Pro	Val	Gly	Ser
				20					25					30		
	Gly	Ala	Tyr	Gly	Ser	Val	Cys	Ala	Ala	Phe	Asp	Thr	Lys	Thr	Gly	Leu
			35					40					45			
5	Arg	Val	Ala	Val	Lys	Lys	Leu	Ser	Arg	Pro	Phe	Gln	Ser	Ile	Ile	His
		50					55					60				
	Ala	Lys	Arg	Thr	Tyr	Arg	Glu	Leu	Arg	Leu	Leu	Lys	His	Met	Lys	His
	65					70					75					80
10	Glu	Asn	Val	Ile	Gly	Leu	Leu	Asp	Val	Phe	Thr	Pro	Ala	Arg	Ser	Leu
					85					90					95	
	Glu	Glu	Phe	Asn	Asp	Val	Tyr	Leu	Val	Thr	His	Leu	Met	Gly	Ala	Asp
				100					105					110		
	Leu	Asn	Asn	Ile	Val	Lys	Cys	Gln	Lys	Leu	Thr	Asp	Asp	His	Val	Gln
			115					120					125			
15	Phe	Leu	Ile	Tyr	Gln	Ile	Leu	Arg	Gly	Leu	Lys	Tyr	Ile	His	Ser	Ala
		130					135					140				
	Asp	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Leu	Ala	Val	Asn	Glu
	145					150					155					160
20	Asp	Cys	Glu	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	His	Thr	Asp
					165					170					175	
	Asp	Glu	Met	Thr	Gly	Tyr	Val	Ala	Thr	Arg	Trp	Tyr	Arg	Ala	Pro	Glu
				180					185					190		
	Ile	Met	Leu	Asn	Trp	Met	His	Tyr	Asn	Gln	Thr	Val	Asp	Ile	Trp	Ser
			195					200					205			
25	Val	Gly	Cys	Ile	Met	Ala	Glu	Leu	Leu	Thr	Gly	Arg	Thr	Leu	Phe	Pro
		210					215					220				
	Gly	Thr	Asp	His	Ile	Asp	Gln	Leu	Lys	Leu	Ile	Leu	Arg	Leu	Val	Gly
	225					230					235					240
30	Thr	Pro	Gly	Ala	Glu	Leu	Leu	Lys	Lys	Ile	Ser	Ser	Glu	Ser	Ala	Arg
					245					250					255	
	Asn	Tyr	Ile	Gln	Ser	Leu	Thr	Gln	Met	Pro	Lys	Met	Asn	Phe	Ala	Asn
				260					265					270		
	Val	Phe	Ile	Gly	Ala	Asn	Pro	Leu	Ala	Val	Asp	Leu	Leu	Glu	Lys	Met
			275					280					285			
35	Leu	Val	Leu	Asp	Ser	Asp	Lys	Arg	Ile	Thr	Ala	Ala	Gln</			

5 Leu Asp Gln Glu Glu Met Glu Ser
 355 360

(2) INFORMATION FOR SEQ ID NO:2:

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10      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 360 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: protein

15      (ix) FEATURE:
          (A) NAME/KEY: Region
          (B) LOCATION: 103..104
          (D) OTHER INFORMATION: /note= "amino acid 103 is
isoleucine or leucine"

20      (ix) FEATURE:
          (A) NAME/KEY: Region
          (B) LOCATION: 105..106
          (D) OTHER INFORMATION: /product= "OTHER"
/note= "amino acid 105 is glutamine, threonine or alanine"

25      (ix) FEATURE:
          (A) NAME/KEY: Region
          (B) LOCATION: 106..107
          (D) OTHER INFORMATION: /product= "OTHER"
/note= "amino acid 106 is aspartic acid or histidine"

30      (ix) FEATURE:
          (A) NAME/KEY: Region
          (B) LOCATION: 109..110
          (D) OTHER INFORMATION: /product= "OTHER"
/note= "amino acid 109 is glutamic acid or glycine"

35      (ix) FEATURE:
          (A) NAME/KEY: Region
          (B) LOCATION: 110..111
          (D) OTHER INFORMATION: /product= "OTHER"
/note= "amino acid 110 is threonine or alanine"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
40 Met Ala Ala Ala Ala Ala Ala Gly Ala Gly Pro Glu Met Val Arg Gly
    1              5              10              15
    Gln Val Phe Asp Val Gly Pro Arg Tyr Thr Asn Leu Ser Tyr Ile Gly
        20              25              30

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[illegible]

Asp Leu Pro Lys Glu Lys Leu Lys Glu Leu Ile Phe Glu Glu Thr Ala
340 345 350

Arg Phe Gln Pro Gly Tyr Arg Ser
355 360

5 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 422 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- 15 (A) NAME/KEY: Region
(B) LOCATION: 146..147
(D) OTHER INFORMATION: /product= "OTHER"
/note= "amino acid 146 is methionine, threonine or alanine"

(ix) FEATURE:

- 20 (A) NAME/KEY: Region
(B) LOCATION: 150..151
(D) OTHER INFORMATION: /product= "OTHER"
/note= "amino acid 150 is aspartic acid or glycine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

25 Met Ser Leu His Phe Leu Tyr Tyr Cys Ser Glu Pro Thr Leu Asp Val
1 5 10 15
Lys Ile Ala Phe Cys Gln Gly Phe Asp Lys Gln Val Asp Val Ser Tyr
20 25 30
Ile Ala Lys His Tyr Asn Met Ser Lys Ser Lys Val Asp Asn Gln Phe
35 40 45
30 Tyr Ser Val Glu Val Gly Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr
50 55 60
Gln Asn Leu Lys Pro Ile Gly Ser Gly Ala Gln Gly Ile Val Cys Ala
65 70 75 80
35 Ala Tyr Asp Ala Val Leu Asp Arg Asn Val Ala Ile Lys Lys Leu Ser
85 90 95
Arg Pro Phe Gln Asn Gln Thr His Ala Lys Arg Ala Tyr Arg Glu Leu
100 105 110
Val Leu Met Lys Cys Val Asn His Lys Asn Ile Ile Ser Leu Leu Asn
115 120 125
40 Val Phe Thr Pro Gln Lys Thr Leu Glu Glu Phe Gln Asp Val Tyr Leu
130 135 140

	Val Xaa Glu Leu Met Xaa Ala Asn Leu Cys Gln Val Ile Gln Met Glu	145	150	155	160
	Leu Asp His Glu Arg Met Ser Tyr Leu Leu Tyr Gln Met Leu Cys Gly		165	170	175
5	Ile Lys His Leu His Ser Ala Gly Ile Ile His Arg Asp Leu Lys Pro		180	185	190
	Ser Asn Ile Val Val Lys Ser Asp Cys Thr Leu Lys Ile Leu Asp Phe		195	200	205
10	Gly Leu Ala Arg Thr Ala Gly Thr Ser Phe Met Met Thr Pro Tyr Val		210	215	220
	Val Thr Arg Tyr Tyr Arg Ala Pro Glu Val Ile Leu Gly Met Gly Tyr		225	230	235
	Lys Glu Asn Val Asp Ile Trp Ser Val Gly Cys Ile Met Gly Glu Met		245	250	255
15	Val Arg His Lys Ile Leu Phe Pro Gly Arg Asp Tyr Ile Asp Gln Trp		260	265	270
	Asn Lys Val Ile Glu Gln Leu Gly Thr Pro Cys Pro Glu Phe Met Lys		275	280	285
20	Lys Leu Gln Pro Thr Val Arg Asn Tyr Val Glu Asn Arg Pro Lys Tyr		290	295	300
	Ala Gly Leu Thr Phe Pro Lys Leu Phe Pro Asp Ser Leu Phe Pro Ala		305	310	315
	Asp Ser Glu His Asn Lys Leu Lys Ala Ser Gln Ala Arg Asp Leu Leu		325	330	335
25	Ser Lys Met Leu Val Ile Asp Pro Ala Lys Arg Ile Ser Val Asp Asp		340	345	350
	Ala Leu Gln His Pro Tyr Ile Asn Val Trp Tyr Asp Pro Ala Glu Val		355	360	365
30	Glu Ala Pro Pro Pro Gln Ile Tyr Asp Lys Gln Leu Asp Glu Arg Glu		370	375	380
	His Thr Ile Glu Glu Trp Lys Glu Leu Ile Tyr Lys Glu Val Met Asn		385	390	395
	Ser Glu Glu Lys Thr Lys Asn Gly Val Val Lys Gly Gln Pro Ser Pro		405	410	415
35	Ser Ala Gln Val Gln Gln		420		

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

10 GAACGGCGGG CAGCCAACAT GGCGGCGGCG 30

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "oligonucleotide"
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(iii) HYPOTHETICAL: NO

20 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGGCTCGAGC CTGACAAATT TAAGATCTGT ATCCTG 36

(2) INFORMATION FOR SEQ ID NO:6:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: other nucleic acid
30      (A) DESCRIPTION: /desc = "oligonucleotide"

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTAACATATG GCGGCGGCGG CGGCGGCG 28

35 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
5 (A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCCACAGGAT CCGATCTGTA TCCTG

25

10 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GATGGTCCGC GGGCAGGTGT TCG

23

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

30 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTGTCTTCAA AAGCTTGTAAGATCTGTTT CC

32

(2) INFORMATION FOR SEQ ID NO:10:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAAAAGCTTG TAAAGATCTG TTTCCATGAG GTCCGTTACT AT

42

(2) INFORMATION FOR SEQ ID NO:11:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

20 CAAAAGCTTG TAAAGATCTG TTTCCATGAG GTCCGCTACT AT

42

(2) INFORMATION FOR SEQ ID NO:12:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: NO

30 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CAAAAGCTTG TAAAGATCTG CTCCCATGAG GTGCGTTACT AGATATAC

48

(2) INFORMATION FOR SEQ ID NO:13:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATCTTTACA AGCTTTTGAA GACACAAC

28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15 (A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTTGGTGTAG CCCTTGGAAT TCAACATA

28

20 (2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

30 (ix) FEATURE:

(A) NAME/KEY: Region

(B) LOCATION: 1..6

(D) OTHER INFORMATION: /note= "C-terminal tag"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

35 Glu Tyr Met Pro Met Glu

1

5

(2) INFORMATION FOR SEQ ID NO:16:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"
- (iii) HYPOTHETICAL: NO

10 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CATGGCACAC CATCACCATC ACCATCCCAA GAAGAAGCCG ACGCCCATCC AG 52

(2) INFORMATION FOR SEQ ID NO:17:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
20 (A) DESCRIPTION: /desc = "oligonucleotide"
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTGGATGGGC GTCGGCTTCT TCTTGGGATG GTGATGGTGA TGGTGTGC 48

25 (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCTCTAGAGC TCCATGGGCA GCAAAAGCAA AGTTGACAA 39

(2) INFORMATION FOR SEQ ID NO:19:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"
- (iii) HYPOTHETICAL: NO
- 10 (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TAGCGGATCC TCATTCTGAA TTCATTACTT CCTTGTA

37

(2) INFORMATION FOR SEQ ID NO:20:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
20 (A) DESCRIPTION: /desc = "oligonucleotide"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCAAGATGTT TACTTAGTAG CGGAAGTAT GGATGCCAA

39

25 (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAAGATGTTT ACTTAGTAAC GGGACTGATG GATGCCAAC

39

(2) INFORMATION FOR SEQ ID NO:22:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
 GTAATGGAAC TGATGGGTGC CAACTTATGT CAAGTG 36

(2) INFORMATION FOR SEQ ID NO:23:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

20 (iv) ANTI-SENSE: NO

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..21
 (D) OTHER INFORMATION: /note= "EGF receptor peptide"

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
 Lys Arg Glu Leu Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn
 1 5 10 15
 Gln Ala Leu Leu Arg
 20

30 (2) INFORMATION FOR SEQ ID NO:24:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 367 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

	Met	Ser	Ser	Pro	Pro	Thr	Arg	Ser	Gly	Phe	Tyr	Arg	Gln	Glu	Val	
	1				5					10					15	
	Thr	Lys	Thr	Ala	Trp	Glu	Val	Arg	Ala	Val	Tyr	Arg	Asp	Leu	Gln	Pro
				20					25					30		
5	Val	Gly	Ser	Gly	Ala	Tyr	Gly	Ala	Val	Cys	Ser	Ala	Val	Asp	Gly	Arg
			35					40					45			
	Thr	Gly	Ala	Lys	Val	Ala	Ile	Lys	Lys	Leu	Tyr	Arg	Pro	Phe	Gln	Ser
		50					55					60				
10	Glu	Leu	Phe	Ala	Lys	Leu	Ala	Tyr	Arg	Glu	Leu	Arg	Leu	Leu	Lys	His
	65					70					75					80
	Met	Arg	His	Glu	Asn	Val	Ile	Gly	Leu	Leu	Asp	Val	Phe	Thr	Pro	Asp
					85					90					95	
	Glu	Thr	Leu	Asp	Asp	Phe	Thr	Asp	Phe	Tyr	Leu	Val	Met	Pro	Phe	Met
				100					105					110		
15	Gly	Thr	Asp	Leu	Gly	Lys	Leu	Met	Lys	His	Glu	Lys	Leu	Gly	Glu	Asp
			115					120					125			
	Arg	Ile	Gln	Phe	Leu	Val	Tyr	Gln	Met	Met	Lys	Gly	Leu	Arg	Tyr	Ile
		130					135					140				
20	His	Ala	Ala	Gly	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Gly	Asn	Leu	Ala
	145					150					155					160
	Val	Asn	Glu	Asp	Cys	Glu	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg
					165					170					175	
	Gln	Ala	Asp	Ser	Glu	Met	Thr	Gly	Tyr	Val	Val	Thr	Arg	Trp	Tyr	Arg
				180					185					190		
25	Ala	Pro	Glu	Val	Ile	Leu	Asn	Trp	Ile	Ala	Tyr	Thr	Gln	Thr	Val	Asp
			195					200					205			
	Ile	Trp	Ser	Val	Gly	Cys	Ile	Met	Ala	Glu	Met	Ile	Thr	Gly	Lys	Thr
		210					215					220				
30	Leu	Phe	Lys	Gly	Ser	Asp	His	Leu	Asp	Gln	Leu	Lys	Glu	Ile	Met	Lys
	225					230					235					240
	Val	Thr	Gly	Thr	Pro	Pro	Ala	Glu	Phe	Val	Gln	Arg	Leu	Gln	Ser	Asp
					245					250					255	
	Glu	Ala	Lys	Asn	Tyr	Met	Lys	Gly	Leu	Pro	Glu	Leu	Glu	Lys	Lys	Asp
				260					265					270		
35	Phe	Ala	Ser	Ile	Leu	Thr	Asn	Ala	Ser	Pro	Leu	Ala	Val	Asn	Leu	Leu

Pro Pro Arg Gln Leu Gly Ala Arg Val Ser Lys Glu Thr Pro Leu
355 360 365

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10      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 379 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Asn Val Leu His Arg Asp Leu Lys Pro Ser Asn Leu Leu Ser Asn Thr
165 170 175

Thr Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Ile Ala Asp
160 185 190

Pro Glu His Asp His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr Arg
195 200 205

5 Trp Tyr Arg Ala Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr Lys
210 215 220

Ser Ile Asp Ile Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu Ser
225 230 235 240

10 Asn Arg Pro Ile Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn His
245 250 255

Ile Leu Gly Ile Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys Ile
260 265 270

Ile Asn Met Lys Ala Arg Asn Tyr Leu Gln Ser Leu Pro Ser Lys Thr
275 280 285

15 Lys Val Ala Trp Ala Lys Leu Phe Pro Lys Ser Asp Ser Lys Ala Leu
290 295 300

Asp Leu Leu Asp Arg Met Leu Thr Phe Asn Pro Asn Lys Arg Ile Thr
305 310 315 320

20 Val Glu Glu Ala Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp Pro
325 330 335

Thr Asp Glu Pro Val Ala Glu Glu Pro Phe Thr Phe Ala Met Glu Leu
340 345 350

Asp Asp Leu Pro Lys Glu Arg Leu Lys Glu Leu Ile Phe Gln Glu Thr
355 360 365

25 Ala Arg Phe Gln Pro Gly Val Leu Glu Ala Pro
370 375

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 365 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

35 Met Ser Leu Ile Arg Lys Lys Gly Phe Tyr Lys Gln Glu Leu Asn Lys
1 5 10 15

Thr Ala Trp Glu Leu Pro Lys Thr Tyr Val Ser Pro Thr His Val Gly
20 25 30

	Ser	Gly	Ala	Tyr	Gly	Ser	Trp	Cys	Ser	Ala	Ile	Asp	Lys	Arg	Ser	Gly	
			35				40						45				
	Glu	Lys	Val	Ala	Ile	Lys	Lys	Leu	Ser	Arg	Pro	Phe	Gln	Ser	Glu	Ile	
		50					55					60					
5	Phe	Ala	Lys	Arg	Ala	Tyr	Arg	Glu	Leu	Leu	Leu	Leu	Lys	His	Met	Gln	
	65					70					75					80	
	His	Glu	Asn	Val	Ile	Gly	Leu	Leu	Asp	Val	Phe	Thr	Pro	Ala	Ser	Ser	
					85					90					95		
10	Leu	Arg	Asn	Phe	Tyr	Asp	Phe	Tyr	Leu	Val	Met	Pro	Phe	Met	Gln	Thr	
				100					105					110			
	Asp	Leu	Gln	Lys	Ile	Met	Gly	Met	Glu	Phe	Ser	Glu	Glu	Lys	Ile	Gln	
			115					120					125				
	Tyr	Leu	Val	Tyr	Gln	Met	Leu	Lys	Gly	Leu	Lys	Tyr	Ile	His	Ser	Ala	
		130					135					140					
15	Gly	Val	Val	His	Arg	Asp	Leu	Lys	Pro	Gly	Asn	Leu	Ala	Val	Asn	Glu	
	145					150					155					160	
	Asp	Cys	Glu	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	His	Ala	Asp	
					165					170					175		
20	Ala	Glu	Met	Thr	Gly	Tyr	Val	Val	Thr	Arg	Trp	Tyr	Arg	Ala	Pro	Glu	
				180					185					190			
	Val	Ile	Leu	Ser	Trp	Met	His	Tyr	Asn	Gln	Thr	Val	Asp	Ile	Trp	Ser	
			195					200					205				
	Val	Gly	Cys	Ile	Met	Ala	Glu	Met	Leu	Thr	Gly	Lys	Thr	Leu	Phe	Lys	
		210					215					220					
25	Gly	Lys	Asp	Tyr	Leu	Asp	Gln	Leu	Thr	Gln	Ile	Leu	Lys	Val	Thr	Gly	
	225					230					235					240	
	Val	Pro	Gly	Thr	Glu	Phe	Val	Gln	Lys	Leu	Asn	Asp	Lys	Ala	Ala	Lys	
					245					250					255		
30	Ser	Tyr	Ile	Gln	Ser	Leu	Pro	Gln	Thr	Pro	Arg	Lys	Asp	Phe	Thr	Gln	
				260					265					270			
	Leu	Phe	Pro	Arg	Ala	Ser	Pro	Gln	Ala	Ala	Asp	Leu	Leu	Glu	Lys	Met	
			275					280					285				
	Leu	Glu	Leu	Asp	Val	Asp	Lys	Arg	Leu	Thr	Ala	Ala	Gln	Ala	Leu	Thr	
		290				295						300					
35	His	Pro	Phe	Phe	Glu	Pro	Phe	Arg	Asp	Pro	Glu	Glu	Glu	Thr	Glu	Ala	
	305					310					315					320	
	Gln	Gln	Pro	Phe	Asp	Asp	Ser	Leu	Glu	His	Glu	Lys	Leu	Thr	Val	Asp	
					325					330					335		

Ala Arg Lys Asp Ser Arg Arg Arg Ser Gly Met Lys Leu
355 360 365

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

	Met	Ser	Leu	Ile	Arg	Lys	Lys	Gly	Phe	Tyr	Lys	Gln	Asp	Val	Asn	Lys
	1					5										15
15	Thr	Ala	Trp	Glu	Leu	Pro	Lys	Thr	Tyr	Val	Ser	Pro	Thr	His	Val	Gly
				20					25					30		
	Ser	Gly	Ala	Tyr	Gly	Ser	Val	Cys	Ser	Ala	Ile	Asp	Lys	Arg	Ser	Gly
			35					40					45			
20	Glu	Lys	Val	Ala	Ile	Lys	Lys	Leu	Ser	Arg	Pro	Phe	Gln	Ser	Glu	Ile
		50					55						60			
	Phe	Ala	Lys	Arg	Ala	Tyr	Arg	Glu	Leu	Leu	Leu	Leu	Lys	His	Met	Gln
	65					70					75					80
	His	Glu	Asn	Val	Ile	Gly	Leu	Leu	Asp	Val	Phe	Thr	Pro	Ala	Ser	Ser
					85					90					95	
25	Leu	Arg	Asn	Phe	Tyr	Asp	Phe	Tyr	Leu	Val	Met	Pro	Phe	Met	Gln	Thr
				100					105					110		
	Asp	Leu	Gln	Lys	Ile	Met	Gly	Met	Glu	Phe	Ser	Glu	Glu	Lys	Ile	Gln
			115					120					125			
30	Tyr	Leu	Val	Tyr	Gln	Met	Leu	Lys	Gly	Leu	Lys	Tyr	Ile	His	Ser	Ala
		130					135					140				
	Gly	Val	Val	His	Arg	Asp	Leu	Lys	Pro	Gly	Asn	Leu	Ala	Val	Asn	Glu
	145					150					155					160
	Asp	Cys	Glu	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	His	Ala	Asp
					165					170					175	
35	Ala	Glu	Met	Thr	Gly	Tyr	Val	Val	Thr	Arg	Trp	Tyr	Arg	Ala	Pro	Glu
				180					185					190		
	Val	Ile	Leu	Ser	Trp	Met	His	Tyr	Asn	Gln	Thr	Val	Asp	Ile	Trp	Ser
			195					200					205			

	Val Gly Cys Ile Met Ala Glu Met Leu Thr Gly Lys Thr Leu Phe Lys	210	215	220
	Gly Lys Asp Tyr Leu Asp Gln Leu Thr Gln Ile Leu Lys Val Thr Gly	225	230	235 240
5	Val Pro Gly Thr Glu Phe Val Gln Lys Leu Asn Asp Lys Ala Ala Lys	245	250	255
	Ser Tyr Ile Gln Ser Leu Pro Gln Thr Pro Arg Lys Asp Phe Thr Gln	260	265	270
10	Leu Phe Pro Arg Ala Ser Pro Gln Ala Ala Asp Leu Leu Glu Lys Met	275	280	285
	Leu Glu Leu Asp Val Asp Lys Arg Leu Thr Ala Ala Gln Ala Leu Thr	290	295	300
	His Pro Phe Phe Glu Pro Phe Arg Asp Pro Glu Glu Glu Thr Glu Ala	305	310	315 320
15	Gln Gln Pro Phe Asp Asp Ser Leu Glu His Glu Lys Leu Thr Val Asp	325	330	335
	Glu Trp Lys Gln His Ile Tyr Lys Glu Ile Val Asn Phe Ser Pro Ile	340	345	350
20	Ala Arg Lys Asp Ser Arg Arg Arg Ser Gly Met Lys Leu	355	360	365

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 464 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

30	Met Ser Leu His Phe Leu Tyr Tyr Cys Ser Glu Pro Thr Leu Asp Val	1	5	10	15
	Lys Ile Ala Phe Cys Gln Gly Phe Asp Lys Gln Val Asp Val Ser Tyr	20	25	30	
	Ile Ala Lys His Tyr Asn Met Ser Lys Ser Lys Val Asp Asn Gln Phe	35	40	45	
35	Tyr Ser Val Glu Val Gly Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr	50	55	60	
	Gln Asn Leu Lys Pro Ile Gly Ser Gly Ala Gln Gly Ile Val Cys Ala	65	70	75	80

	Ala Tyr Asp Ala Val Leu Asp Arg Asn Val Ala Ile Lys Lys Leu Ser	85	90	95
	Arg Pro Phe Gln Asn Gln Thr His Ala Lys Arg Ala Tyr Arg Glu Leu	100	105	110
5	Val Leu Met Lys Cys Val Asn His Lys Asn Ile Ile Ser Leu Leu Asn	115	120	125
	Val Phe Thr Pro Gln Lys Thr Leu Glu Glu Phe Gln Asp Val Tyr Leu	130	135	140
10	Val Met Glu Leu Met Asp Ala Asn Leu Cys Gln Val Ile Gln Met Glu	145	150	155
	Leu Asp His Glu Arg Met Ser Tyr Leu Leu Tyr Gln Met Leu Cys Gly	165	170	175
	Ile Lys His Leu His Ser Ala Gly Ile Ile His Arg Asp Leu Lys Pro	180	185	190
15	Ser Asn Ile Val Val Lys Ser Asp Cys Thr Leu Lys Ile Leu Asp Phe	195	200	205
	Gly Leu Ala Arg Thr Ala Gly Thr Ser Phe Met Met Thr Pro Tyr Val	210	215	220
20	Val Thr Arg Tyr Tyr Arg Ala Pro Glu Val Ile Leu Gly Met Gly Tyr	225	230	235
	Lys Glu Asn Val Asp Ile Trp Ser Val Gly Cys Ile Met Gly Glu Met	245	250	255
	Val Arg His Lys Ile Leu Phe Pro Gly Arg Asp Tyr Ile Asp Gln Trp	260	265	270
25	Asn Lys Val Ile Glu Gln Leu Gly Thr Pro Cys Pro Glu Phe Met Lys	275	280	285
	Lys Leu Gln Pro Thr Val Arg Asn Tyr Val Glu Asn Arg Pro Lys Tyr	290	295	300
30	Ala Gly Leu Thr Phe Pro Lys Leu Phe Pro Asp Ser Leu Phe Pro Ala	305	310	315
	Asp Ser Glu His Asn Lys Leu Lys Ala Ser Gln Ala Arg Asp Leu Leu	325	330	335
	Ser Lys Met Leu Val Ile Asp Pro Ala Lys Arg Ile Ser Val Asp Asp	340	345	350
35	Ala Leu Gln His Pro Tyr Ile Asn Val Trp Tyr Asp Pro Ala Glu Val	355	360	365
	Glu Ala Pro Pro Pro Gln Ile Tyr Asp Lys Gln Leu Asp Glu Arg Glu	370	375	380

Ser Glu Glu Lys Thr Lys Asn Gly Val Val Lys Gly Gln Pro Ser Pro
405 410 415

5 Ser Gly Ala Ala Val Asn Ser Ser Glu Ser Leu Pro Pro Ser Ser Ser
 420 425 430

Val Asn Asp Ile Ser Ser Met Ser Thr Asp Gln Thr Leu Ala Ser Asp
435 440 445

Thr Asp Ser Ser Leu Glu Ala Ser Ala Gly Pro Leu Gly Cys Cys Arg
10 450 455 460

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Ser Asp Ser Lys Cys Asp Ser Gln Phe Tyr Ser Val Gln Val Ala
20 1 5 10 15

Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr Gln Gln Leu Lys Pro Ile
20 25 30

Gly Ser Gly Ala Gln Gly Ile Val Cys Ala Ala Phe Asp Thr Val Leu
35 40 45

25 Gly Ile Ser Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Asn Gln
50 55 60

Thr His Ala Lys Arg Ala Tyr Arg Glu Leu Val Leu Leu Lys Cys Val
65 70 75 80

Asn His Lys Asn Ile Ile Ser Leu Leu Asn Val Phe Thr Pro Gln Lys
30 85 90 95

Thr Leu Glu Glu Phe Gln Asp Val Tyr Leu Val Met Glu Leu Met Asp
100 105 110

Ala Asn Leu Cys Gln Val Ile His Met Glu Leu Asp His Glu Arg Met
115 120 125

[illegible]

Ala Gly Ile Ile His Arg Asp Leu Lys Pro Ser Asn Ile Val Val Lys
145 150 155 160

	Ser	Asp	Cys	Thr	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	Thr	Ala	
					165					170					175		
	Cys	Anr	Asn	Phe	Met	Met	Thr	Pro	Tyr	Val	Val	Thr	Arg	Tyr	Tyr	Arg	
				180					185					190			
5	Ala	Pro	Glu	Val	Ile	Leu	Gly	Met	Gly	Tyr	Lys	Glu	Asn	Val	Asp	Ile	
			195					200					205				
	Trp	Ser	Val	Gly	Cys	Ile	Met	Gly	Glu	Leu	Val	Lys	Gly	Cys	Val	Ile	
			210				215						220				
10	Phe	Gln	Gly	Thr	Asp	His	Ile	Asp	Gln	Trp	Asn	Lys	Val	Ile	Glu	Gln	
						230					235					240	
	Leu	Gly	Thr	Pro	Ser	Ala	Glu	Phe	Met	Lys	Lys	Leu	Gln	Pro	Thr	Val	
						245				250					255		
	Arg	Asn	Tyr	Val	Glu	Asn	Arg	Pro	Lys	Tyr	Pro	Gly	Ile	Lys	Phe	Glu	
				260					265					270			
15	Glu	Leu	Phe	Pro	Asp	Trp	Ile	Phe	Pro	Ser	Glu	Ser	Glu	Arg	Asp	Lys	
			275					280					285				
	Ile	Lys	Thr	Ser	Gln	Ala	Arg	Asp	Leu	Leu	Ser	Lys	Met	Leu	Val	Ile	
			290				295					300					
20	Asp	Pro	Asp	Lys	Arg	Ile	Ser	Val	Asp	Glu	Ala	Leu	Arg	His	Pro	Tyr	
		305				310					315					320	
	Ile	Thr	Val	Trp	Tyr	Asp	Pro	Ala	Glu	Ala	Glu	Ala	Pro	Pro	Pro	Gln	
					325					330					335		
	Ile	Tyr	Asp	Ala	Gln	Leu	Glu	Glu	Arg	Glu	His	Ala	Ile	Glu	Glu	Trp	
				340					345					350			
25	Lys	Glu	Leu	Ile	Tyr	Lys	Glu	Val	Met	Asp	Trp	Glu	Glu	Arg	Ser	Lys	
			355					360					365				
	Asn	Gly	Val	Val	Lys	Asp	Gln	Pro	Ser	Ala	Gln	Met	Gln	Gln			
			370				375					380					

(2) INFORMATION FOR SEQ ID NO:30:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 382 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met	Ser	Asp	Ser	Lys	Cys	Asp	Ser	Gln	Phe	Tyr	Ser	Val	Gln	Val	Ala
1				5					10					15	

	Asp	Ser	Thr	Phe	Thr	Val	Leu	Lys	Arg	Tyr	Gln	Gln	Leu	Lys	Pro	Ile	
				20					25					30			
	Gly	Ser	Gly	Ala	Gln	Gly	Ile	Val	Cys	Ala	Ala	Phe	Asp	Thr	Val	Leu	
			35					40					45				
5	Gly	Ile	Ser	Val	Ala	Val	Lys	Lys	Leu	Ser	Arg	Pro	Phe	Gln	Asn	Gln	
		50					55					60					
	Thr	His	Ala	Lys	Arg	Ala	Tyr	Arg	Glu	Leu	Val	Leu	Leu	Lys	Cys	Val	
	65					70					75					80	
10	Asn	His	Lys	Asn	Ile	Ile	Ser	Leu	Leu	Asn	Val	Phe	Thr	Pro	Gln	Lys	
				85						90					95		
	Thr	Leu	Glu	Glu	Phe	Gln	Asp	Val	Tyr	Leu	Val	Met	Glu	Leu	Met	Asp	
				100					105					110			
	Ala	Asn	Leu	Cys	Gln	Val	Ile	His	Met	Glu	Leu	Asp	His	Glu	Arg	Met	
			115					120					125				
15	Ser	Tyr	Leu	Leu	Tyr	Gln	Met	Leu	Cys	Gly	Ile	Lys	His	Leu	His	Ser	
		130					135					140					
	Ala	Gly	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Ile	Val	Val	Lys	
	145					150					155					160	
20	Ser	Asp	Cys	Thr	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	Thr	Ala	
					165					170					175		
	Cys	Thr	Asn	Phe	Met	Met	Thr	Pro	Tyr	Val	Val	Thr	Arg	Tyr	Tyr	Arg	
				180					185					190			
	Ala	Pro	Glu	Val	Ile	Leu	Gly	Met	Gly	Tyr	Lys	Glu	Asn	Val	Asp	Ile	
			195					200					205				
25	Trp	Ser	Val	Gly	Cys	Ile	Met	Ala	Glu	Met	Val	Leu	His	Lys	Val	Leu	
		210					215					220					
	Phe	Pro	Gly	Arg	Asp	Tyr	Ile	Asp	Gln	Trp	Asn	Lys	Val	Ile	Glu	Gln	
	225					230					235					240	
30	Leu	Gly	Thr	Pro	Ser	Ala	Glu	Phe	Met	Lys	Lys	Leu	Gln	Pro	Thr	Val	
					245					250					255		
	Arg	Asn	Tyr	Val	Glu	Asn	Arg	Pro	Lys	Tyr	Pro	Gly	Ile	Lys	Phe	Glu	
				260					265					270			
	Glu	Leu	Phe	Pro	Asp	Trp	Ile	Phe	Pro	Ser	Glu	Ser	Glu	Arg	Asp	Lys	
			275					280					285				
35	Ile	Lys	Thr	Ser	Gln	Ala	Arg	Asp	Leu	Leu	Ser	Lys	Met	Leu	Val	Ile	
		290					295					300					
	Asp	Pro	Asp	Lys	Arg	Ile	Ser	Val	Asp	Glu	Ala	Leu	Arg	His	Pro	Tyr	
	305					310					315					320	

005750: 6442450

Ile Thr Val Trp Tyr Asp Pro Ala Glu Ala Glu Ala Pro Pro Pro Gln
325 330 335

Ile Tyr Asp Ala Gln Leu Glu Glu Arg Glu His Ala Ile Glu Glu Trp
340 345 350

5 Lys Glu Leu Ile Tyr Lys Glu Val Met Asp Trp Glu Glu Arg Ser Lys
355 360 365

Asn Gly Val Val Lys Asp Gln Pro Ser Ala Gln Met Gln Gln
370 375 380

(2) INFORMATION FOR SEQ ID NO:31:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 424 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Ser Asp Ser Lys Cys Asp Ser Gln Phe Tyr Ser Val Gln Val Ala
1 5 10 15

20 Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr Gln Gln Leu Lys Pro Ile
20 25 30

Gly Ser Gly Ala Gln Gly Ile Val Cys Ala Ala Phe Asp Thr Val Leu
35 40 45

Gly Ile Ser Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Asn Gln
50 55 60

25 Thr His Ala Lys Arg Ala Tyr Arg Glu Leu Val Leu Leu Lys Cys Val
65 70 75 80

Asn His Lys Asn Ile Ile Ser Leu Leu Asn Val Phe Thr Pro Gln Lys
85 90 95

30 Thr Leu Glu Glu Phe Gln Asp Val Tyr Leu Val Met Glu Leu Met Asp
100 105 110

Ala Asn Leu Cys Gln Val Ile His Met Glu Leu Asp His Glu Arg Met
115 120 125

Ser Tyr Leu Leu Tyr Gln Met Leu Cys Gly Ile Lys His Leu His Ser
130 135 140

35 Ala Gly Ile Ile His Arg Asp Leu Lys Pro Ser Asn Ile Val Val Lys
145 150 155 160

Ser Asp Cys Thr Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg Thr Ala
165 170 175

	Cys	Thr	Asn	Phe	Met	Met	Thr	Pro	Tyr	Val	Val	Thr	Arg	Tyr	Tyr	Arg
				180					185					190		
	Ala	Pro	Glu	Val	Ile	Leu	Gly	Met	Gly	Tyr	Lys	Glu	Asn	Val	Asp	Ile
			195					200					205			
5	Trp	Ser	Val	Gly	Cys	Ile	Met	Ala	Glu	Met	Val	Leu	His	Lys	Val	Leu
		210					215					220				
	Phe	Pro	Gly	Arg	Asp	Tyr	Ile	Asp	Gln	Trp	Asn	Lys	Val	Ile	Glu	Gln
	225					230					235					240
10	Leu	Gly	Thr	Pro	Ser	Ala	Glu	Phe	Met	Lys	Lys	Leu	Gln	Pro	Thr	Val
						245				250					255	
	Arg	Asn	Tyr	Val	Glu	Asn	Arg	Pro	Lys	Tyr	Pro	Gly	Ile	Lys	Phe	Glu
				260					265					270		
	Glu	Leu	Phe	Pro	Asp	Trp	Ile	Phe	Pro	Ser	Glu	Ser	Glu	Arg	Asp	Lys
			275					280					285			
15	Ile	Lys	Thr	Ser	Gln	Ala	Arg	Asp	Leu	Leu	Ser	Lys	Met	Leu	Val	Ile
		290					295					300				
	Asp	Pro	Asp	Lys	Arg	Ile	Ser	Val	Asp	Glu	Ala	Leu	Arg	His	Pro	Tyr
	305					310					315					320
20	Ile	Thr	Val	Trp	Tyr	Asp	Pro	Ala	Glu	Ala	Glu	Ala	Pro	Pro	Pro	Gln
					325					330					335	
	Ile	Tyr	Asp	Ala	Gln	Leu	Glu	Glu	Arg	Glu	His	Ala	Ile	Glu	Glu	Trp
				340					345					350		
	Lys	Glu	Leu	Ile	Tyr	Lys	Glu	Val	Met	Asp	Trp	Glu	Glu	Arg	Ser	Lys
			355					360					365			
25	Asn	Gly	Val	Val	Lys	Asp	Gln	Pro	Ser	Asp	Ala	Ala	Val	Ser	Ser	Asn
		370					375					380				
	Ala	Thr	Pro	Ser	Gln	Ser	Ser	Ser	Ile	Asn	Asp	Ile	Ser	Ser	Met	Ser
	385					390					395					400
30	Thr	Glu	Gln	Thr	Leu	Ala	Ser	Asp	Thr	Asp	Ser	Ser	Leu	Asp	Ala	Ser
					405					410					415	
	Thr	Gly	Pro	Leu	Glu	Gly	Cys	Arg								
					420											

(2) INFORMATION FOR SEQ ID NO:32:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 424 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

	Met	Ser	Asp	Ser	Lys	Cys	Asp	Ser	Gln	Phe	Tyr	Ser	Val	Gln	Val	Ala	
	1				5					10					15		
5	Asp	Ser	Thr	Phe	Thr	Val	Leu	Lys	Arg	Tyr	Gln	Gln	Leu	Lys	Pro	Ile	
				20					25					30			
	Gly	Ser	Gly	Ala	Gln	Gly	Ile	Val	Cys	Ala	Ala	Phe	Asp	Thr	Val	Leu	
			35					40					45				
	Gly	Ile	Asn	Val	Ala	Val	Lys	Lys	Leu	Ser	Arg	Pro	Phe	Gln	Asn	Gln	
		50					55					60					
10	Thr	His	Ala	Lys	Arg	Ala	Tyr	Arg	Glu	Leu	Val	Leu	Leu	Lys	Cys	Val	
	65					70					75					80	
	Asn	His	Lys	Asn	Ile	Ile	Ser	Leu	Leu	Asn	Val	Phe	Thr	Pro	Gln	Lys	
				85						90					95		
15	Thr	Leu	Glu	Glu	Phe	Gln	Asp	Val	Tyr	Leu	Val	Met	Glu	Leu	Met	Asp	
				100					105					110			
	Ala	Asn	Leu	Cys	Gln	Val	Ile	His	Met	Glu	Leu	Asp	His	Glu	Arg	Met	
			115					120					125				
	Ser	Tyr	Leu	Leu	Tyr	Gln	Met	Leu	Cys	Gly	Ile	Lys	His	Leu	His	Ser	
		130					135					140					
20	Ala	Gly	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Ile	Val	Val	Lys	
	145					150					155					160	
	Ser	Asp	Cys	Thr	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	Thr	Ala	
				165						170					175		
25	Cys	Thr	Asn	Phe	Met	Met	Thr	Pro	Tyr	Val	Val	Thr	Arg	Tyr	Tyr	Arg	
			180						185					190			
	Ala	Pro	Glu	Val	Ile	Leu	Gly	Met	Gly	Tyr	Lys	Glu	Asn	Val	Asp	Ile	
			195					200					205				
	Trp	Ser	Val	Gly	Cys	Ile	Met	Gly	Glu	Leu	Val	Lys	Gly	Cys	Val	Ile	
		210					215						220				
30	Phe	Gln	Gly	Thr	Asp	His	Ile	Asp	Gln	Trp	Asn	Lys	Val	Ile	Glu	Gln	
	225					230					235					240	
	Leu	Gly	Thr	Pro	Ser	Ala	Glu	Phe	Met	Lys	Lys	Leu	Gln	Pro	Thr	Val	
				245						250					255		
35	Arg	Asn	Tyr	Val	Glu	Asn	Arg	Pro	Lys	Tyr	Pro	Gly	Ile	Lys	Phe	Glu	
			260						265					270			
	Glu	Leu	Phe	Pro	Asp	Trp	Ile	Phe	Pro	Ser	Glu	Ser	Glu	Arg	Asp	Lys	
			275					280					285				
	Ile	Lys	Thr	Ser	Gln	Ala	Arg	Asp	Leu	Leu	Ser	Lys	Met	Leu	Val	Ile	
		290					295						300				

Asp Pro Asp Lys Arg Ile Ser Val Asp Glu Ala Leu Arg His Pro Tyr
305 310 315 320

Ile Thr Val Trp Tyr Asp Pro Ala Glu Ala Glu Ala Pro Pro Pro Gln
325 330 335

5 Ile Tyr Asp Ala Gln Leu Glu Glu Arg Glu His Ala Ile Glu Glu Trp
340 345 350

Lys Glu Leu Ile Tyr Lys Glu Val Met Asp Trp Glu Glu Arg Ser Lys
355 360 365

10 Asn Gly Val Val Lys Asp Gln Pro Pro Asp Ala Ala Val Ser Ser Asn
370 375 380

Ala Thr Pro Ser Gln Ser Ser Ser Ile Asn Asp Ile Ser Ser Met Ser
385 390 395 400

Thr Glu Gln Thr Leu Ala Ser Asp Thr Asp Ser Ser Leu Asp Ala Ser
405 410 415

15 Thr Gly Pro Leu Glu Gly Cys Arg
420

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 384 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

25 Met Ser Arg Ser Lys Arg Asp Asn Asn Phe Tyr Ser Val Glu Ile Gly
1 5 10 15

Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr Gln Asn Leu Lys Pro Ile
20 25 30

30 Gly Ser Gly Ala Gln Gly Ile Val Cys Ala Ala Tyr Asp Ala Ile Leu
35 40 45

Glu Arg Asn Val Ala Ile Lys Lys Leu Ser Arg Pro Phe Gln Asn Gln
50 55 60

Thr His Ala Lys Arg Ala Tyr Arg Glu Leu Val Leu Met Lys Cys Val
65 70 75 80

35 Asn His Lys Asn Ile Ile Gly Leu Leu Asn Val Phe Thr Pro Gln Lys
85 90 95

Ser Leu Glu Glu Phe Gln Asp Val Tyr Ile Val Met Glu Leu Met Asp
100 105 110

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

5	Met	Ser	Arg	Ser	Lys	Arg	Asp	Asn	Asn	Phe	Tyr	Ser	Val	Glu	Ile	Gly	1	5	10	15
	Asp	Ser	Thr	Phe	Thr	Val	Leu	Lys	Arg	Tyr	Gln	Asn	Leu	Lys	Pro	Ile	20	25	30	
	Gly	Ser	Gly	Ala	Gln	Gly	Ile	Val	Cys	Ala	Ala	Tyr	Asp	Ala	Ile	Leu	35	40	45	
10	Glu	Arg	Asn	Val	Ala	Ile	Lys	Lys	Leu	Ser	Arg	Pro	Phe	Gln	Asn	Gln	50	55	60	
	Thr	His	Ala	Lys	Arg	Ala	Tyr	Arg	Glu	Leu	Val	Leu	Met	Lys	Cys	Val	65	70	75	80
15	Asn	His	Lys	Asn	Ile	Ile	Gly	Leu	Leu	Asn	Val	Phe	Thr	Pro	Gln	Lys	85	90	95	
	Ser	Leu	Glu	Glu	Phe	Gln	Asp	Val	Tyr	Ile	Val	Met	Glu	Leu	Met	Asp	100	105	110	
	Ala	Asn	Leu	Cys	Gln	Val	Ile	Gln	Met	Glu	Leu	Asp	His	Glu	Arg	Met	115	120	125	
20	Ser	Tyr	Leu	Leu	Tyr	Gln	Met	Leu	Cys	Gly	Ile	Lys	His	Leu	His	Ser	130	135	140	
	Ala	Gly	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Ile	Val	Val	Lys	145	150	155	160
25	Ser	Asp	Cys	Thr	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	Thr	Ala	165	170	175	
	Gly	Thr	Ser	Phe	Met	Met	Thr	Pro	Tyr	Val	Val	Thr	Arg	Tyr	Tyr	Arg	180	185	190	
	Ala	Pro	Glu	Val	Ile	Leu	Gly	Met	Gly	Tyr	Lys	Glu	Asn	Val	Asp	Leu	195	200	205	
30	Trp	Ser	Val	Gly	Cys	Ile	Met	Gly	Glu	Met	Val	Cys	His	Lys	Ile	Leu	210	215	220	
	Phe	Pro	Gly	Arg	Asp	Tyr	Ile	Asp	Gln	Trp	Asn	Lys	Val	Ile	Glu	Gln	225	230	235	240
35	Leu	Gly	Thr	Pro	Cys	Pro	Glu	Phe	Met	Lys	Lys	Leu	Gln	Pro	Thr	Val	245	250	255	
	Arg	Thr	Tyr	Val	Glu	Asn	Arg	Pro	Lys	Tyr	Ala	Gly	Tyr	Ser	Phe	Glu	260	265	270	

	Lys	Leu	Phe	Pro	Asp	Val	Leu	Phe	Pro	Ala	Asp	Ser	Glu	His	Asn	Lys	
	Leu	Lys	Ala	Ser	Gln	Ala	Arg	Asp	Leu	Leu	Ser	Lys	Met	Leu	Val	Ile	
	290						295					300					
5	Asp	Ala	Ser	Lys	Arg	Ile	Ser	Val	Asp	Glu	Ala	Leu	Gln	His	Pro	Tyr	
	305					310					315					320	
	Ile	Asn	Val	Trp	Tyr	Asp	Pro	Ser	Glu	Ala	Glu	Ala	Pro	Pro	Pro	Lys	
					325					330					335		
10	Ile	Pro	Asp	Lys	Gln	Leu	Asp	Glu	Arg	Glu	His	Thr	Ile	Glu	Glu	Trp	
				340					345					350			
	Lys	Glu	Leu	Ile	Tyr	Lys	Glu	Val	Met	Asp	Leu	Glu	Glu	Arg	Thr	Lys	
			355					360					365				
	Asn	Gly	Val	Ile	Arg	Gly	Gln	Pro	Ser	Pro	Leu	Gly	Ala	Ala	Val	Ile	
		370					375					380					
15	Asn	Gly	Ser	Gln	His	Pro	Ser	Ser	Ser	Ser	Ser	Val	Asn	Asp	Val	Ser	
	385					390					395					400	
	Ser	Met	Ser	Thr	Asp	Pro	Thr	Leu	Ala	Ser	Asp	Thr	Asp	Ser	Ser	Leu	
					405					410					415		
20	Glu	Ala	Ala	Ala	Gly	Pro	Leu	Gly	Cys	Cys	Arg						
				420					425								

(2) INFORMATION FOR SEQ ID NO:35:

	(i) SEQUENCE CHARACTERISTICS:																
	(A) LENGTH: 384 amino acids																
	(B) TYPE: amino acid																
25	(C) STRANDEDNESS: single																
	(D) TOPOLOGY: linear																
	(ii) MOLECULE TYPE: protein																
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:																
30	Met	Ser	Arg	Ser	Lys	Arg	Asp	Asn	Asn	Phe	Tyr	Ser	Val	Glu	Ile	Gly	
	1				5					10					15		
	Asp	Ser	Thr	Phe	Thr	Val	Leu	Lys	Arg	Tyr	Gln	Asn	Leu	Lys	Pro	Ile	
				20					25					30			
	Gly	Ser	Gly	Ala	Gln	Gly	Ile	Val	Cys	Ala	Ala	Tyr	Asp	Ala	Ile	Leu	
			35				40						45				
35	Glu	Arg	Asn	Val	Ala	Ile	Lys	Lys	Leu	Ser	Arg	Pro	Phe	Gln	Asn	Gln	
		50					55				60						
	Thr	His	Ala	Lys	Arg	Ala	Tyr	Arg	Glu	Leu	Val	Leu	Met	Lys	Cys	Val	
	65					70					75					80	

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	Asn	His	Lys	Asn	Ile	Ile	Gly	Leu	Leu	Asn	Val	Phe	Thr	Pro	Gln	Lys
					85					90					95	
	Ser	Leu	Glu	Glu	Phe	Gln	Asp	Val	Tyr	Ile	Val	Met	Glu	Leu	Met	Asp
			100						105					110		
5	Ala	Asn	Leu	Cys	Gln	Val	Ile	Gln	Met	Glu	Leu	Asp	His	Glu	Arg	Met
			115					120					125			
	Ser	Tyr	Leu	Leu	Tyr	Gln	Met	Leu	Cys	Gly	Ile	Lys	His	Leu	His	Ser
		130				135						140				
10	Ala	Gly	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Ile	Val	Val	Lys
	145					150					155					160
	Ser	Asp	Cys	Thr	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	Thr	Ala
					165					170					175	
	Gly	Thr	Ser	Phe	Met	Met	Thr	Pro	Tyr	Val	Val	Thr	Arg	Tyr	Tyr	Arg
				180					185					190		
15	Ala	Pro	Glu	Val	Ile	Leu	Gly	Met	Gly	Tyr	Lys	Glu	Asn	Val	Asp	Ile
			195					200					205			
	Trp	Ser	Val	Gly	Cys	Ile	Met	Gly	Glu	Met	Ile	Lys	Gly	Gly	Val	Leu
		210					215					220				
20	Phe	Pro	Gly	Thr	Asp	His	Ile	Asp	Gln	Trp	Asn	Lys	Val	Ile	Glu	Gln
	225					230					235					240
	Leu	Gly	Thr	Pro	Cys	Pro	Glu	Phe	Met	Lys	Lys	Leu	Gln	Pro	Thr	Val
					245					250					255	
	Arg	Thr	Tyr	Val	Glu	Asn	Arg	Pro	Lys	Tyr	Ala	Gly	Tyr	Ser	Phe	Glu
				260					265					270		
25	Lys	Leu	Phe	Pro	Asp	Val	Leu	Phe	Pro	Ala	Asp	Ser	Glu	His	Asn	Lys
			275					280					285			
	Leu	Lys	Ala	Ser	Gln	Ala	Arg	Asp	Leu	Leu	Ser	Lys	Met	Leu	Val	Ile
		290					295					300				
30	Asp	Ala	Ser	Lys	Arg	Ile	Ser	Val	Asp	Glu	Ala	Leu	Gln	His	Pro	Tyr
	305					310					315					320
	Ile	Asn	Val	Trp	Tyr	Asp	Pro	Ser	Glu	Ala	Glu	Ala	Pro	Pro	Pro	Lys
					325					330					335	
	Ile	Pro	Asp	Lys	Gln	Leu	Asp	Glu	Arg	Glu	His	Thr	Ile	Glu	Glu	Trp
				340					345					350		
35	Lys	Glu	Leu	Ile	Tyr	Lys	Glu	Val	Met	Asp	Leu	Glu	Glu	Arg	Thr	Lys
		355						360					365			
	Asn	Gly	Val	Ile	Arg	Gly	Gln	Pro	Ser	Pro	Leu	Ala	Gln	Val	Gln	Gln
		370					375					380				

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 427 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

10 Met Ser Arg Ser Lys Arg Asp Asn Asn Phe Tyr Ser Val Glu Ile Gly
1 5 10 15

Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr Gln Asn Leu Lys Pro Ile
20 25 30

Gly Ser Gly Ala Gln Gly Ile Val Cys Ala Ala Tyr Asp Ala Ile Leu
35 40 45

15 Glu Arg Asn Val Ala Ile Lys Lys Leu Ser Arg Pro Phe Gln Asn Gln
50 55 60

Thr His Ala Lys Arg Ala Tyr Arg Glu Leu Val Leu Met Lys Cys Val
65 70 75 80

20 Asn His Lys Asn Ile Ile Gly Leu Leu Asn Val Phe Thr Pro Gln Lys
85 90 95

Ser Leu Glu Glu Phe Gln Asp Val Tyr Ile Val Met Glu Leu Met Asp
100 105 110

Ala Asn Leu Cys Gln Val Ile Gln Met Glu Leu Asp His Glu Arg Met
115 120 125

25 Ser Tyr Leu Leu Tyr Gln Met Leu Cys Gly Ile Lys His Leu His Ser
130 135 140

Ala Gly Ile Ile His Arg Asp Leu Lys Pro Ser Asn Ile Val Val Lys
145 150 155 160

30 Ser Asp Cys Thr Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg Thr Ala
165 170 175

Gly Thr Ser Phe Met Met Thr Pro Tyr Val Val Thr Arg Tyr Tyr Arg
180 185 190

Ala Pro Glu Val Ile Leu Gly Met Gly Tyr Lys Glu Asn Val Asp Ile
195 200 205

35 Trp Ser Val Gly Cys Ile Met Gly Glu Met Ile Lys Gly Gly Val Leu
210 215 220

Phe Pro Gly Thr Asp His Ile Asp Gln Trp Asn Lys Val Ile Glu Gln
225 230 235 240

Leu Gly Thr Pro Cys Pro Glu Phe Met Lys Lys Leu Gln Pro Thr Val
245 250 255

Arg Thr Tyr Val Glu Asn Arg Pro Lys Tyr Ala Gly Tyr Ser Phe Glu
260 265 270

5 Lys Leu Phe Pro Asp Val Leu Phe Pro Ala Asp Ser Glu His Asn Lys
275 280 285

Leu Lys Ala Ser Gln Ala Arg Asp Leu Leu Ser Lys Met Leu Val Ile
290 295 300

10 Asp Ala Ser Lys Arg Ile Ser Val Asp Glu Ala Leu Gln His Pro Tyr
305 310 315 320

Ile Asn Val Trp Tyr Asp Pro Ser Glu Ala Glu Ala Pro Pro Pro Lys
325 330 335

Ile Pro Asp Lys Gln Leu Asp Glu Arg Glu His Thr Ile Glu Glu Trp
340 345 350

15 Lys Glu Leu Ile Tyr Lys Glu Val Met Asp Leu Glu Glu Arg Thr Lys
355 360 365

Asn Gly Val Ile Arg Gly Gln Pro Ser Pro Leu Gly Ala Ala Val Ile
370 375 380

20 Asn Gly Ser Gln His Pro Ser Ser Ser Ser Val Asn Asp Val Ser
385 390 395 400

Ser Met Ser Thr Asp Pro Thr Leu Ala Ser Asp Thr Asp Ser Ser Leu
405 410 415

Glu Ala Ala Ala Gly Pro Leu Gly Cys Cys Arg
420 425

25 (2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 364 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Ser Gly Pro Arg Ala Gly Phe Tyr Arg Gln Glu Leu Asn Lys Thr
1 5 10 15

35 Val Trp Glu Val Pro Gln Arg Leu Gln Gly Leu Arg Pro Val Gly Ser
20 25 30

Gly Ala Tyr Gly Ser Val Cys Ser Ala Tyr Asp Ala Arg Leu Arg Gln
35 40 45

	Lys	Val	Ala	Val	Lys	Lys	Leu	Ser	Arg	Pro	Phe	Gln	Ser	Leu	Ile	His
	50						55					60				
	Ala	Arg	Arg	Thr	Tyr	Arg	Glu	Leu	Arg	Leu	Leu	Lys	His	Leu	Lys	His
	65					70					75					80
5	Glu	Asn	Val	Ile	Gly	Leu	Leu	Asp	Val	Phe	Thr	Pro	Ala	Thr	Ser	Ile
					85					90					95	
	Glu	Asp	Phe	Ser	Glu	Val	Tyr	Leu	Val	Thr	Thr	Leu	Met	Gly	Ala	Asp
				100					105					110		
10	Leu	Asn	Asn	Ile	Val	Lys	Cys	Gln	Ala	Leu	Ser	Asp	Glu	His	Val	Gln
			115					120					125			
	Phe	Leu	Val	Tyr	Gln	Leu	Leu	Arg	Gly	Leu	Lys	Tyr	Ile	His	Ser	Ala
	130					135						140				
	Gly	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Val	Ala	Val	Asn	Glu
	145					150					155					160
15	Asp	Cys	Glu	Leu	Arg	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	Gln	Ala	Asp
					165					170					175	
	Glu	Glu	Met	Thr	Gly	Tyr	Val	Ala	Thr	Arg	Trp	Tyr	Arg	Ala	Pro	Glu
				180					185					190		
20	Ile	Met	Leu	Asn	Trp	Met	His	Tyr	Asn	Gln	Thr	Val	Asp	Ile	Trp	Ser
			195					200					205			
	Val	Gly	Cys	Ile	Met	Ala	Glu	Leu	Leu	Gln	Gly	Lys	Ala	Leu	Phe	Pro
		210					215					220				
	Gly	Ser	Asp	Tyr	Ile	Asp	Gln	Leu	Lys	Arg	Ile	Met	Glu	Val	Val	Gly
	225					230					235					240
25	Thr	Pro	Ser	Pro	Glu	Val	Leu	Ala	Lys	Ile	Ser	Ser	Glu	His	Ala	Arg
					245					250					255	
	Thr	Tyr	Ile	Gln	Ser	Leu	Pro	Pro	Met	Pro	Gln	Lys	Asp	Leu	Ser	Ser
				260					265					270		
30	Ile	Phe	Arg	Gly	Ala	Asn	Pro	Leu	Ala	Ile	Asp	Leu	Leu	Gly	Arg	Met
			275					280					285			
	Leu	Val	Leu	Asp	Ser	Asp	Gln	Arg	Val	Ser	Ala	Ala	Glu	Ala	Leu	Ala
		290					295					300				
	His	Ala	Tyr	Phe	Ser	Gln	Tyr	His	Asp	Pro	Glu	Asp	Glu	Pro	Glu	Ala
	305					310					315					320
35	Glu	Pro	Tyr	Asp	Glu	Gly	Val	Glu	Ala	Lys	Glu	Arg	Thr	Leu	Glu	Glu
					325					330					335	
	Trp	Lys	Glu	Leu	Thr	Tyr	Gln	Glu	Val	Leu	Ser	Phe	Lys	Pro	Pro	Glu
				340					345					350		

[illegible]